

Relative Resistance of HLA-B to Downregulation by Naturally Occurring HIV-1 Nef Sequences

Macdonald Mahiti,^{a,b} Mako Toyoda,^a Xiaofei Jia,^c Xiaomei T. Kuang,^d Francis Mwimanzi,^a Philip Mwimanzi,^{a,d} Bruce D. Walker,^{e,f,g} Yong Xiong,^c Zabrina L. Brumme,^{d,h} Mark A. Brockman,^{d,h}  Takamasa Ueno^{a,b}

Center for AIDS Research^a and International Research Center for Medical Sciences (IRCMS),^b Kumamoto University, Kumamoto, Japan; Department of Molecular Biophysics and Biochemistry, Yale University, New Haven, Connecticut, USA^c; Simon Fraser University, Burnaby, British Columbia, Canada^d; Ragon Institute of MGH, MIT and Harvard University, Boston, Massachusetts, USA^e; Division of Infectious Diseases, Massachusetts General Hospital, Boston, Massachusetts, USA^f; Howard Hughes Medical Institute, Chevy Chase, Maryland, USA^g; British Columbia Centre for Excellence in HIV/AIDS, Vancouver, British Columbia, Canada^h

M. M. and M. T. contributed equally to this work.

ABSTRACT HIV-1 Nef binds to the cytoplasmic region of HLA-A and HLA-B and downregulates these molecules from the surface of virus-infected cells, thus evading immune detection by CD8⁺ T cells. Polymorphic residues within the HLA cytoplasmic region may affect Nef's downregulation activity. However, the effects of HLA polymorphisms on recognition by primary Nef isolates remain elusive, as do the specific Nef regions responsible for downregulation of HLA-A versus HLA-B. Here, we examined 46 Nef clones isolated from chronically HIV-1 subtype B-infected subjects for their ability to downregulate various HLA-A, HLA-B, and HLA-C molecules on the surface of virus-infected cells. Overall, HLA-B exhibited greater resistance to Nef-mediated downregulation than HLA-A, regardless of the cell type examined. As expected, no Nef clone downregulated HLA-C. Importantly, the differential abilities of patient-derived Nef clones to downregulate HLA-A and HLA-B correlated inversely with the sensitivities of HIV-infected target cells to recognition by effector cells expressing an HIV-1 Gag-specific T cell receptor. Nef codon function analysis implicated amino acid variation at position 202 (Nef-202) in differentially affecting the ability to downregulate HLA-A and HLA-B, an observation that was subsequently confirmed by experiments using Nef mutants constructed by site-directed mutagenesis. The *in silico* and mutagenesis analyses further suggested that Nef-202 may interact with the C-terminal Cys-Lys-Val residues of HLA-A, which are absent in HLA-B. Taken together, the results show that natural polymorphisms within Nef modulate its interaction with natural polymorphisms in the HLA cytoplasmic tails, thereby affecting the efficiency of HLA downregulation and consequent recognition by HIV-specific T cells. These results thus extend our understanding of this complex pathway of retroviral immune evasion.

IMPORTANCE Recognition of genetically diverse pathogens by the adaptive immune system represents a primary strategy for host defense; however, pathogens such as HIV-1 can evade these responses to achieve persistent infection. The HIV-1 *nef* gene and the *HLA class I* locus rank among the most diverse genes of virus and host, respectively. The HIV-1 Nef protein interacts with the cytoplasmic region of HLA-A and HLA-B and downregulates these molecules to evade cellular immunity. By combining molecular, genetic, and *in silico* analyses, we demonstrate that patient-derived Nef clones downregulate HLA-A more effectively than HLA-B molecules. This in turn modulates the ability of HIV-specific T cells to recognize HIV-infected cells. We also identify a naturally polymorphic site at Nef codon 202 and HLA cytoplasmic motifs (GG_{314,315} and CKV₃₃₉₋₃₄₁) that contribute to differential HLA downregulation by Nef. Our results highlight new interactions between HIV-1 and the human immune system that may contribute to pathogenesis.

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Address correspondence to Takamasa Ueno, uenotaka@kumamoto-u.ac.jp.

The HLA class I (HLA-I) gene region, comprising the *HLA-A*, *HLA-B*, and *HLA-C* loci, ranks among the most polymorphic regions in the human genome, with 2,735 *HLA-A*, 3,455 *HLA-B*, and 2,259 *HLA-C* alleles identified to date (International ImMunoGeneTics project [IMGT] HLA database; <http://www.ebi.ac.uk/ipd/imgt/hla/>) (see reviews in references 1 and 2). HLA-I polymorphism is mainly concentrated within exons 2 and 3 (1), which primarily form the antigenic peptide-binding groove of the

HLA-I complex (3) and play an important role in restricting CD8⁺ T lymphocyte specificity. Other exons also exhibit polymorphism, albeit to a lesser extent. For example, *HLA-A*, *HLA-B*, and *HLA-C* alleles can be classified into 5, 2, and 7 polymorphic types, respectively, based on sequence variations within their cytoplasmic domains (encoded by exons 5 to 7 for *HLA-B* or 5 through 8 for *HLA-A* and *HLA-C*). Polymorphism in the cytoplasmic domain also influences receptor expression: for example,

a unique amino acid conserved in all HLA-C allotypes (Ile at codon 337 [Ile-337], rather than Thr-337 as in HLA-A and HLA-B) yields lower cell surface expression of HLA-C than of HLA-A and HLA-B (4). However, the implications of HLA cytoplasmic polymorphisms for modulation of antiviral immunity remain incompletely understood.

HLA-I-restricted CD8⁺ cytotoxic T lymphocyte (CTL) responses are important for controlling a wide range of viral infections (5, 6), including HIV-1 (7, 8), human T-cell leukemia virus type 1 (HTLV-1) (9), cytomegalovirus (10), and herpes simplex virus (11) infections. In turn, viruses have evolved various mechanisms to evade HLA-I-restricted antiviral immunity, such as inhibiting intracellular antigen-processing pathways and downregulating HLA-I molecules from the infected cell surface (see reviews in references 12 to 14). In HIV-1, the 27- to 35-kDa accessory protein Nef downregulates HLA-A and HLA-B molecules from the surface of HIV-1-infected cells (15, 16). Nef does not downregulate HLA-C molecules due to the presence of unique residues at codons 320 and 327 in their cytoplasmic regions (17). As such, the antiviral activities of HLA-A and HLA-B-restricted CTLs are substantially reduced by Nef expression (18–20), whereas the antiviral activities of HLA-C-restricted CTLs are unaffected by Nef (21). Maintenance of HLA-C expression allows virus-infected cells to escape recognition by the innate immune system, as downregulation of all HLA-I molecules would render HIV-infected cells susceptible to recognition by natural killer cells (22). Importantly, it was recently demonstrated that chimeric HLA-A02 molecules expressing various HLA-A and HLA-B cytoplasmic tails are differentially susceptible to Nef-mediated downregulation and that this in turn has implications for infected-cell recognition by HLA-A02-restricted CTLs (23). However, all prior studies focused on a limited number of prototypic laboratory-adapted HIV-1 strains (22, 23). It is thus unclear whether highly diverse naturally occurring (patient-derived) Nef sequences also display differential abilities to downregulate HLA-A and HLA-B, and if so, which Nef residue(s) modulate these interactions.

Nef ranks among the most diverse HIV-1 proteins (24, 25). Primary Nef clones isolated from patients at various infection stages and/or with different disease phenotypes exhibit substantial functional heterogeneity (26–31), including wide-ranging HLA-I downregulation capacities (26, 28–30, 32–35). However, previous studies investigated a variety of HLA-I allotypes using different target cells and antibodies; as such, the possibility that these differences were influenced in part by the experimental conditions cannot be conclusively ruled out. In this study, we assessed 46 subtype B Nef clones isolated from the same number of chronically HIV-1-infected patients for their ability to downregulate various HLA-A, HLA-B, and HLA-C allotypes. Individual primary Nef clones exhibited differential abilities to downregulate HLA-I allotypes, with HLA-B molecules exhibiting decreased susceptibility to Nef-mediated downregulation compared to the susceptibility of HLA-A (whereas HLA-C was resistant to Nef's effects). Differential Nef-mediated downregulation of HLA-A versus HLA-B molecules in turn modulated the ability of HIV-specific effector T cells to recognize HIV-infected target cells. By combining statistical analysis, site-specific mutagenesis, and structural interpretation, we identified natural polymorphisms within Nef and HLA cytoplasmic sequences that contribute to Nef's differential abilities to downregulate HLA-A and HLA-B molecules.

RESULTS

Differential downregulation of HLA-A, HLA-B, and HLA-C by HIV-1 laboratory strains. To investigate differential downregulation of various HLA-A, HLA-B, and HLA-C allotypes by HIV-1 Nef, we stably transfected HLA class I-deficient 721.221 cells with HLA-A*02:01 (A02), HLA-A*24:02 (A24), HLA-A*33:01 (A33), HLA-B*35:01 (B35), HLA-B*57:01 (B57), or HLA-C*04:01 (C04). The cytoplasmic tails of HLA-B molecules are 3 amino acids shorter than those of HLA-A and HLA-C molecules (Fig. 1A). Moreover, HLA-A allotypes harbor aspartic acid and arginine at codons 314 and 315, respectively (DR_{314,315}), whereas HLA-B and HLA-C allotypes harbor dual glycines (GG_{314,315}). There are additional amino acid differences between individual allotypes within the cytoplasmic regions (Fig. 1A). The cell surface expression of HLA-I molecules on 721.221 cells was stable and substantial (Fig. 1B, top row). Specifically, the levels of surface expression of the three HLA-A (A02, A24, and A33) and two HLA-B (B35 and B57) allotypes were comparable when cells were stained with the pan-HLA-specific monoclonal antibody (MAb) w6/32, whereas the surface expression of the HLA-C allotype (C04) was lower, as expected. No changes in cell surface HLA-I expression were observed in cells infected with the HIV-1 reference strain NL43 engineered to lack Nef (NL43-ΔNef) (Fig. 1B, middle row). In contrast, when cells were infected with vesicular stomatitis virus envelope glycoprotein (VSV-g)-pseudotyped HIV-1 NL43 expressing the Nef gene from the prototypic laboratory strain SF2 (NL43-Nef_{SF2}), all HLA-A and HLA-B allotypes were downregulated from the cell surface, whereas the HLA-C allotype was unaffected (Fig. 1B, bottom row). As described in Materials and Methods, HLA-I downregulation activity was quantified using a scale from 0% (denoting no HLA-I downregulation activity in virus-infected cells) to 100% (denoting complete downregulation activity). The greater the downregulation activity value, the lower the residual cell surface expression of HLA-I. Nef_{SF2}'s ability to downregulate individual HLA-A and HLA-B molecules varied to some extent; the downregulation values (mean ± standard deviation [SD]), by allotype, were 71.4% ± 3.1% for A02, 61.2% ± 3.7% for A24, 57.4% ± 2.4% for A33, 50.1% ± 2.4% for B35, and 52.4% ± 3.1% for B57 (Fig. 1C). Importantly, Nef_{SF2}'s ability to downregulate HLA-A alleles consistently exceeded that of HLA-B (Mann-Whitney test, $P < 0.001$). Two other laboratory HIV-1 Nef strains, Nef_{NL43} and Nef_{JRFL}, were also evaluated for their ability to downregulate A24 and B35 (see Fig. S1 in the supplemental material). In both cases, their ability to downregulate HLA-A exceeded their ability to downregulate HLA-B (Mann-Whitney, $P < 0.001$), and neither downregulated C04.

Differential downregulation of HLA-A, HLA-B, and HLA-C by natural Nef sequences. We next assessed whether patient-derived Nef sequences differed in their ability to downregulate HLA-A, HLA-B, and HLA-C allotypes. For these experiments, we used 721.221 cells stably expressing A24, B35, and C04 as allotype representatives. A24 and B35 were chosen because they exhibited levels of susceptibility to Nef-mediated downregulation similar to the median values of the HLA-A and HLA-B allotypes tested (Fig. 1C), while C04 was chosen because the 721.221 cells expressing this allele exhibited the most stable cell surface HLA-C expression among our panel of 721.221 cells engineered to express various HLA-C allotypes. Representative HLA-I downregulation

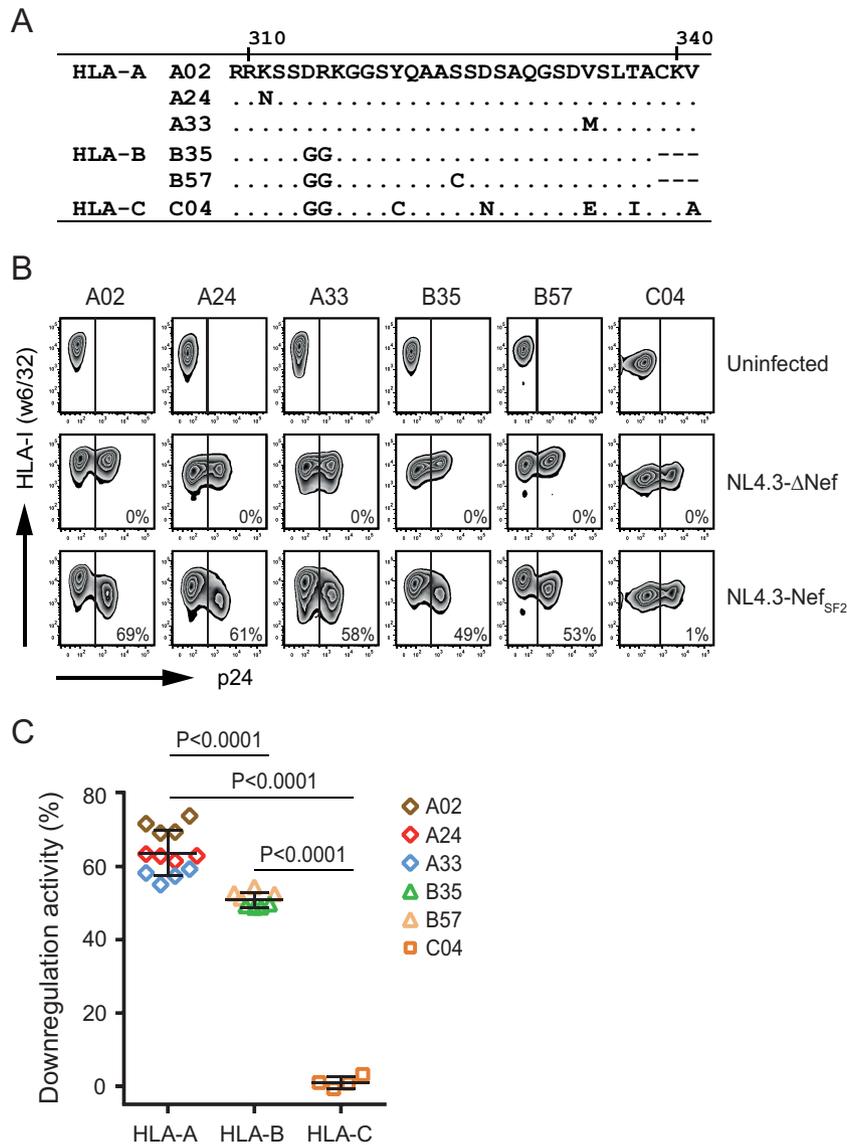


FIG 1 Downregulation of HLA-A, HLA-B, and HLA-C by laboratory Nef strain SF2. (A) Amino acid sequences of the cytoplasmic tails of HLA-A*02:01 (A02), HLA-A*24:02 (A24), HLA-A*33:01 (A33), HLA-B*35:01 (B35), HLA-B*57:01 (B57), and HLA-C*04:01 (C04) proteins. Dots denote amino acid residues identical to A02, and dashes denote the absence of amino acids at those positions. (B) HLA-I-deficient 721.221 cells stably transfected with the indicated HLA-I molecule were infected with recombinant HIV-1 lacking Nef (Δ Nef) or carrying Nef_{SF2}. Uninfected cultures were also used as controls. The cells were stained with an antibody to HLA class I (clone w6/32), followed by intracellular staining with an antibody to p24 Gag. Nef-mediated HLA downregulation activities are shown on the flow cytometry plots. These values were calculated as the difference in levels of HLA-I mean fluorescence intensity between the p24-negative and the p24-positive subsets divided by that of the p24-negative subset. (C) Quantitative assessment of Nef_{SF2}-mediated downregulation activity toward HLA-A, HLA-B, and HLA-C alleles. Symbols denote measurements obtained from experiments performed in quadruplicate. Horizontal bars denote median values and interquartile ranges. The Mann-Whitney *U* test was used to calculate statistical significance.

data, derived from cells infected with HIV-1 NL43-derived strains encoding Nef clonal sequences from three chronic progressors (subjects CP66, CP84, and CP90) are shown in Fig. 2A. The three patient-derived Nef clones varied in their ability to downregulate A24 and B35, but none downregulated C04. For example, CP66-Nef's B35 downregulation activity was 23%, which was approximately half of that of Nef_{SF2} (49%, Fig. 1B). In contrast, CP84-Nef's A24 and B35 downregulation activities, 66% and 56%, respectively, were comparable to those of Nef_{SF2}. CP90-Nef downregulated A24 and B35 by equivalent, relatively lower levels (38% and 41%, respectively).

To quantify the ability of naturally occurring Nef sequences to downregulate A24 and B35, we expanded this analysis to 46 patient-derived Nef clones. All 46 Nef clones displayed greater ability to downregulate A24 (median activity of 60.8% [interquartile range {IQR}, 54.2 to 65.5]) than B35 (median activity, 49.3% [IQR, 41.0 to 55.5]) (Fig. 2B), a difference that was highly statistically significant (Mann-Whitney, *P* < 0.001). No clone downregulated C04. To quantify each virus' ability to differentially downregulate A24 versus B35, we expressed the downregulation values as pairwise ratios. Overall, the median ratio of A24/B35 downregulation activities of patient-derived Nef clones was 1.25

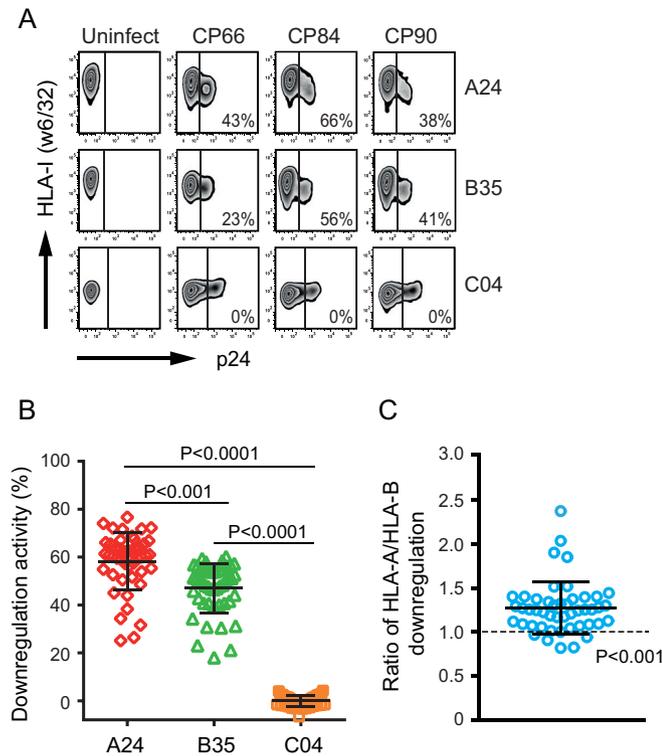


FIG 2 Downregulation of HLA-A, HLA-B, and HLA-C by primary Nef clones. (A) 721.221 transfectants expressing A24, B35, or C04 were infected with recombinant viruses carrying Nef clones isolated from 46 HIV-infected patients. Three sets of representative flow cytometry plots, for the Nef clones from patients CP66, CP84, and CP90, are shown. Nef-mediated HLA-I downregulation activities determined as described above are indicated in the plots. (B) HLA-I downregulation activities by 46 patient-derived Nef clones in 721.221 transfectants expressing A24, B35, or C04 are shown. Bars and whiskers denote median results and interquartile ranges. Each plot represents the mean results from 3 or 4 independent assays. Statistical analysis was done by Mann-Whitney *U* test. (C) Ratios of levels of downregulation activity of A24 and B35 by 46 primary Nef isolates are shown. Bars and whiskers denote median results and interquartile ranges. Dotted line represents the null expectation of a ratio of 1.0. Statistical analysis was done by Wilcoxon one-sample test.

(IQR, 1.09 to 1.37), a value that differed significantly from the null expectation of a ratio of 1.0 (Wilcoxon one-sample test, $P < 0.001$) (Fig. 2C).

Cells normally express two different allomorphs each of HLA-A, HLA-B, and HLA-C (homozygotes excepted). As such, a maximum of four different HLA-A and HLA-B allomorphs normally compete for Nef binding in infected cells (which differs from our 721.221 cell system, where HLA alleles are expressed

singly). We therefore tested Nef-mediated downregulation of HLA-A and HLA-B in the T1 human CD4⁺ cell line that endogenously expresses four different HLA-A and HLA-B alleles (see Materials and Methods). Among them, HLA-A*02:01 (A02) and HLA-B*51:01 (B51) are specifically detectable by MAbs for the HLA-A2 serotype (clone BB7.2) and alleles belonging to the HLA-Bw4 serotype group (clone TU109), respectively. The cytoplasmic tails of A02 and A24 differ by a single amino acid (Fig. 1A), whereas those of B51 and B35 are identical. Again, Nef_{SF2} downregulated A02 more potently than B51 in T1 cells, with activities (mean \pm SD) of 60.3% \pm 1.6% and 51.6% \pm 3.4%, respectively (*t* test, $P < 0.0001$). Moreover, all 46 patient-derived Nef clones downregulated A02 (median, 58.3% [IQR, 54.5 to 63.2]) more potently than B51 (median, 47.7% [IQR, 44.2 to 50.7]) (Mann-Whitney test, $P < 0.0001$) (see Fig. S2A in the supplemental material). These values yielded a median ratio of A02/B51 downregulation in T1 cells by patient-derived Nef of 1.24 [IQR 1.18 to 1.29] (see Fig. S2B), which was again significantly different from the null expectation of a ratio of 1.0 (Wilcoxon one-sample test, $P < 0.001$).

HIV-1 Nef codons associated with differential HLA-A and HLA-B downregulation We next performed a pairwise Nef codon function analysis to identify Nef amino acid residues associated with A24 and B35 downregulation. At the predefined threshold of a *P* value of < 0.05 and a *q* value of < 0.2 , no Nef residues were identified as being associated with A24 or B35 downregulation ability (data not shown). However, when the analysis was performed using the A24/B35 downregulation ratio as the functional variable, Nef clones carrying Glu-158 exhibited significantly higher A24/B35 downregulation ratios than those carrying another amino acid at this site ($P = 0.00064$, $q = 0.13$). In contrast, Nef clones carrying Tyr-202 exhibited significantly lower ratios than those carrying another amino acid at this site ($P = 0.0017$, $q = 0.17$) (Table 1). Using the T1 cell results as an independent validation data set, we confirmed that Tyr-202 was significantly associated with lower ratios (Mann-Whitney, $P = 0.04$), while Glu-158 showed a trend toward higher ratios, although this was not statistically significant ($P = 0.11$). These results suggested that the amino acid residues at HIV-1 Nef codons 158 and 202 may play a role in this protein's differential recognition of HLA-A versus HLA-B allotypes.

Variation at Nef-202 modulates HLA-A and HLA-B downregulation. To examine the effects of amino acid residues at codons 158 and 202 on selective downregulation of HLA-A and HLA-B, we introduced various amino acid substitutions into Nef_{SF2} at these sites and analyzed the function of the mutant viruses. We introduced Ala, His, Lys, and Met substitutions at codon 158 (wild-type Glu) and Ala, His, Leu, and Phe substitu-

TABLE 1 Nef amino acid residues associated with differential HLA-A/HLA-B downregulation ratios in 721.221 cells

Nef codon ^a	Amino acid	HLA-A/HLA-B downregulation ratio for Nef clone ^b :		No. of subjects whose Nef clone ^c :		<i>P</i> value	<i>q</i> value
		With residue	Without residue	Had residue	Did not have residue		
158	Glu	1.30	1.07	33	12	0.00064	0.13
202	Tyr	1.23	1.65	40	6	0.0017	0.17

^a Nef codon numbers are based on the sequence of Nef_{HXB2}.

^b Median HLA-A*24/HLA-B*35 downregulation activity ratio.

^c The row total varies due to the gap in the aligned sequence.

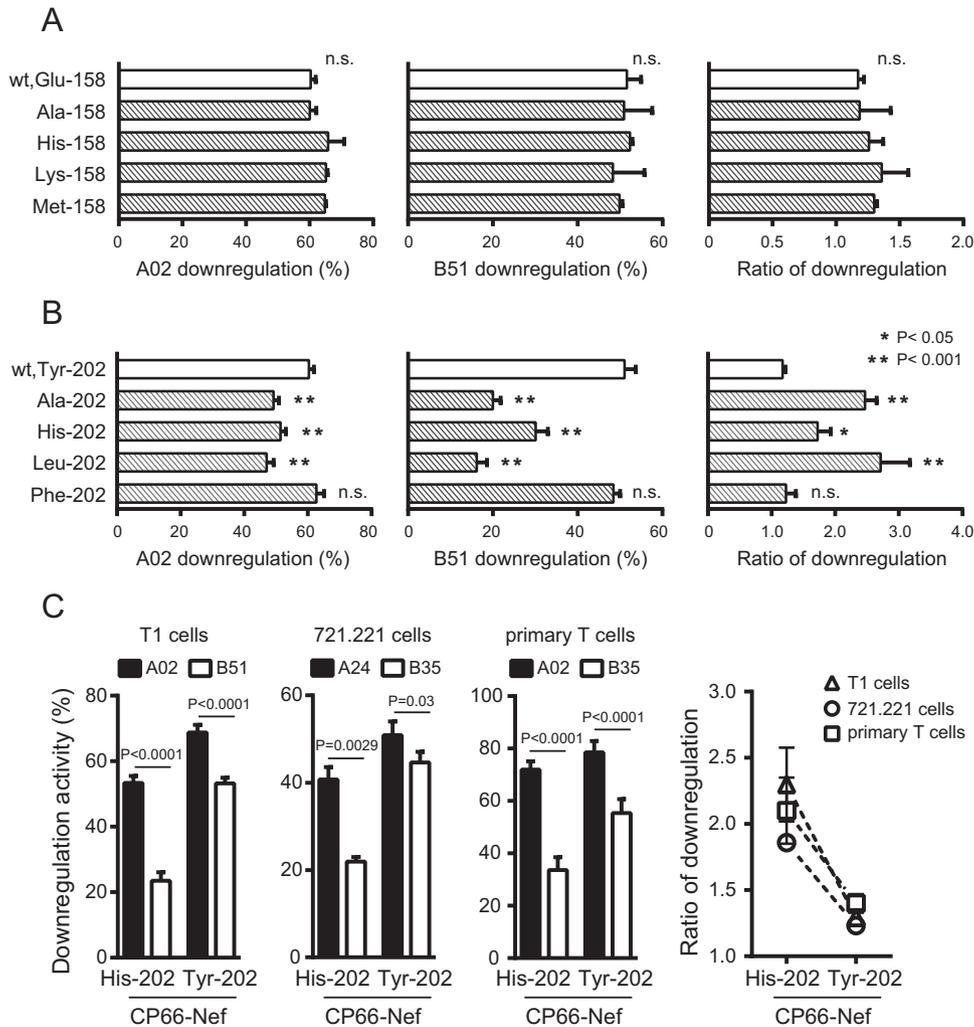


FIG 3 Effects of defined Nef mutations on HLA-A and HLA-B downregulation activity. (A and B) Nef_{SF2} and its variants at position 158 (A) and 202 (B) were tested for downregulation activity toward A02 and B51 in T1 cells. The ratios of the results for A02 and B51 were also determined. Data shown are the mean results \pm SD from 3 or 4 independent experiments. Statistical analysis was performed by analysis of variance (ANOVA) with multiple comparisons versus the results for the wild type (wt). n.s., not significant. (C) CP66-Nef clones encoding His-202 and Tyr-202 were tested for downregulation activity in T1 cells (for A02 and B51), 721.221 cells (for A24 and B35), and human primary T lymphocytes isolated from an HIV-negative donor (expressing A02 and B35). The ratios of HLA-A and HLA-B downregulation activities are also shown. Data shown are the mean results \pm SD from 3 or 4 independent experiments. Statistical analysis was performed by paired *t* test. Similar data were obtained using primary T lymphocytes isolated from another HIV-negative donor.

tions at codon 202 (wild-type Tyr). These substitutions included naturally occurring residues (Ala, Lys, and Met at 158 and His, Leu, and Phe at 202), as well as residues not observed in natural Nef sequences (His at 158 and Ala at 202), as determined in our cohort and in 1,470 publically available subtype B Nef sequences in the Los Alamos HIV sequence database. The steady-state levels of the wild-type Nef protein and the variants were comparable in virus-producing cells (data not shown). We then tested the Nef variants for A02 and B51 downregulation activity in T1 cells. No mutation at codon 158 substantially influenced A02 or B51 downregulation activity or A02/B51 downregulation ratios (Fig. 3A). In contrast, all mutations at codon 202, except Phe, significantly decreased Nef-mediated downregulation of both A02 and B51 in T1 cells compared to the downregulation activity of wild-type Tyr-202 (Fig. 3B). Moreover, these mutations impaired B51 downregulation activity to a greater extent than they impaired A02

downregulation, resulting in corresponding A02/B51 downregulation ratios that were also significantly higher (Fig. 3B). Specifically, the A02/B51 downregulation ratios for the Ala-, His-, and Leu-202 mutations were 2.47 ± 0.18 , 1.72 ± 0.21 , and 2.55 ± 0.42 , respectively, values that were 2.1-, 1.5- and 2.2-fold higher, respectively, than that of wild-type Nef_{SF2} (Tyr-202). Consistent results were also obtained in 721.221 cells expressing A24 and B35 (see Fig. S3 in the supplemental material).

To further confirm the effect of Nef-202 on differential HLA-A and HLA-B downregulation, we introduced a His-to-Tyr mutation into patient CP66's Nef clone at codon 202, thereby reverting this clone to the wild-type sequence at this position. This particular patient clone was chosen because it exhibited substantially impaired HLA-B downregulation activity in T1 cells (A02/B51 downregulation ratio, 2.30 ± 0.28), 721.221 cells (A24/B35 downregulation ratio, 1.86 ± 0.04), and primary T cells (A02/B35

downregulation ratio, 2.16 ± 0.25) (Fig. 3C). The introduction of the His-to-Tyr reversion substantially increased A02 and B51 downregulation activity in T1 cells, A24 and B35 downregulation activity in 721.221 cells, and A02 and B35 downregulation activity in primary T cells (Fig. 3C). As the extent of functional rescue by this reversion was more pronounced for HLA-B than for HLA-A allotypes, the ratio of HLA-A/HLA-B downregulation activities of CP66-Nef decreased to 1.29 ± 0.06 in T1 cells, 1.23 ± 0.01 in 721.221 cells, and 1.43 ± 0.07 in primary T cells, values that are comparable to the median for patient-derived Nef clones (Fig. 2C). These data indicate that amino acid polymorphism at Nef-202 alone can modulate Nef's ability to downregulate HLA-B and, to a lesser extent, HLA-A allotypes.

HLA-I cytoplasmic motifs that modulate sensitivity to Nef-mediated downregulation. Nef-mediated downregulation of cell surface HLA-I molecules occurs through interaction between the HLA cytoplasmic domain and Nef in conjunction with the clathrin adaptor protein complex 1 (AP1) (17, 36, 37). We sought to identify HLA-I cytoplasmic motifs that determine sensitivity to Nef-mediated downregulation. As shown by the sequences in Fig. 1A, HLA-A and HLA-B alleles differ in their amino acid residues at codons 314 and 315, as well as in the presence (HLA-A) or absence (HLA-B) of the C-terminal Cys-Lys-Val (CKV_{339–341}) motif. We therefore created a chimeric A02 molecule possessing the cytoplasmic tail of B35 by introducing a GG_{314,315} mutation into A02 and additionally deleting its C-terminal CKV_{339–341} motif; we designated this sequence A02_{GG,ΔCKV}. We then established Jurkat T cells stably expressing A02 and A02_{GG,ΔCKV}, which exhibited similar cell surface expression of these molecules upon staining with anti-HLA-A2 serotype antibody (mean fluorescence intensities [MFI], $5,664 \pm 226$ and $4,989 \pm 263$, respectively) (Fig. 4A). Infection of these cells with an HIV-1 NL43 strain encoding Nef_{SF2} resulted in downregulation of A02 and A02_{GG,ΔCKV} to similar levels (Fig. 4A and B). As expected, the introduction of the His-202 mutation into Nef_{SF2} impaired its ability to downregulate both A02 and A02_{GG,ΔCKV}, to a greater extent for the latter. Specifically, the introduction of His-202 increased the A02/A02_{GG,ΔCKV} downregulation ratio from 1.03 to 1.82, a 1.8-fold increase (Fig. 4C). Complementary results were obtained with the parental (His-202) and wild-type revertant (Tyr-202) CP66-Nef sequences. Specifically, the CP66 Tyr-202 revertant mutant exhibited A02 downregulation activity comparable to that of Nef_{SF2} and A02_{GG,ΔCKV} downregulation activity moderately lower than that of Nef_{SF2} (Fig. 4A and B). In contrast, the parental CP66-Nef (His-202) exhibited substantially impaired A02_{GG,ΔCKV} downregulation activity. Overall, the Tyr-to-His substitution increased the A02/A02_{GG,ΔCKV} downregulation ratio of CP66-Nef from 1.15 to 2.86, a 2.5-fold increase (Fig. 4C).

We further investigated potential interactions between Nef codon 202 and the cytoplasmic tails of A02 and A02_{GG,ΔCKV} by examining the existing crystal structure of the A02 cytoplasmic tail and Nef in complex with the $\mu 1$ subunit of AP1 (37). This crystal structure exhibits an involvement of Tyr-202 of Nef in contacting a portion of the $\mu 1$ subunit of AP1 and forming a part of the groove for HLA-I binding (Fig. 5A and B) (37). Although the crystal structure did not include A02's cytoplasmic tail in its entirety (the last residue observed in the structure is Gly-331, which lies seven residues upstream from the C-terminal CKV_{339–341} that is present in A02 but absent in HLA-B alleles, since the remaining region is disordered in three-dimensional space), the proximity of

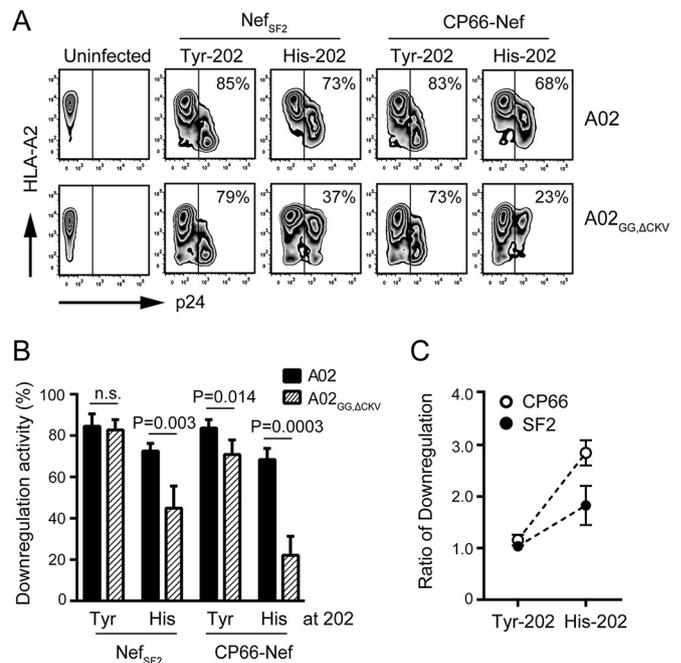


FIG 4 Effects of HLA-I cytoplasmic tail polymorphisms on Nef-mediated HLA-A and HLA-B downregulation activity. (A) The amino acid sequence of the cytoplasmic region of A02 was mutated to encode GG_{314,315} and a C-terminal deletion mutant of the CKV_{339–341} motif, resulting in a cytoplasmic sequence identical to that of B35 (A02_{GG,ΔCKV}; see Fig. 1A). Jurkat transfectants stably expressing A02 and A02_{GG,ΔCKV} were infected with recombinant NL43 viruses encoding various Nef clones or remained uninfected. The Nef clones tested were Nef_{SF2} with Tyr-202 or His-202 and CP66-Nef with Tyr-202 or His-202. Representative flow cytometry plots are shown, and the levels of HLA downregulation activity are indicated in the plots. (B and C) Quantitative assessment of the downregulation activities (B) and the activity ratios (C) of A02 and A02_{GG,ΔCKV} are shown. The data shown are the mean results \pm SD from 3 to 5 independent assays. Statistical analysis was performed by paired *t* test. n.s., not significant.

Gly-331 to the main chain atoms of Nef Tyr-202 suggested that CKV_{339–341} could also be located nearby. Indeed, modeling of a 7-amino-acid spacer following Gly-331 indicated that CKV_{339–341} could readily be positioned next to the side chain of Nef Tyr-202 for potential interaction (Fig. 5B). In contrast, the DR_{314,315} residues of HLA-A, present in the crystal structure, do not directly contact any Nef residues (Fig. 5A). These data suggest that Nef codon 202 and the C-terminal CKV_{339–341} motif that is present in HLA-A but not HLA-B alleles, in conjunction with the $\mu 1$ subunit of clathrin AP1, may form an interaction that enhances the downregulation of HLA-A over that of HLA-B.

Effects on T cell recognition. We postulated that Nef's differential abilities to downregulate HLA-A and HLA-B molecules would have consequences for T cell recognition of viral antigens presented on the surface of HIV-infected cells (18–20, 35). To test this hypothesis, we used a published reporter cell coculture assay that features HLA-A*02:01-expressing target cells and HIV-1-specific effector cells that transiently express a T-cell receptor (TCR) specific for an HLA-A*02:01-restricted HIV-1 epitope in Gag (FK10; Gag_{433–442} [FLGKIWPSYK]), human CD8- α chain, and an nuclear factor of activated T cells (NFAT)-driven luciferase construct (see Materials and Methods). When target cells are infected with HIV, endogenously derived viral peptide antigens are

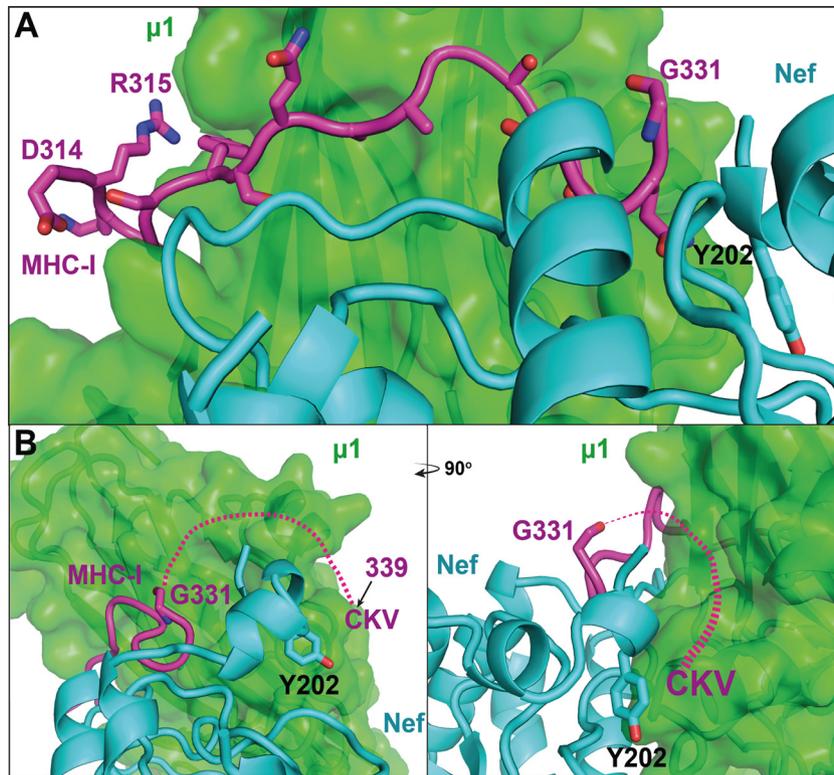


FIG 5 Structural analysis of interaction between HLA-I cytoplasmic tail and Nef. (A) Interactions between A02 cytoplasmic domain, Nef, and $\mu 1$ subunit of adaptor protein 1 (AP1) are illustrated based on coordinates from the tripartite structure (PDB code 4EN2). The DR_{314,315} motif in the HLA-A cytoplasmic domain, which corresponds to GG_{314,315} in the HLA-B cytoplasmic domain, is indicated. The C terminus of HLA-A was not observed in the structure; however, the last observed C-terminal residue, G331, is located close to Nef Tyr-202. (B) Modeling suggests that the CKV_{339–341} motif may be located in the vicinity of the side chain of Nef Tyr-202, allowing it to make a molecular contact. The dotted line depicts a potential path of the 7 amino acids, SDVSLTA, leading from G331 to the terminal CKV_{339–341} motif in HLA-A. MHC-I, major histocompatibility complex class I.

processed and presented in complex with A02 on their surface, though the HIV Nef protein counteracts this by downregulating HLA-I. When HIV-infected target cells are cocultured with A02-FK10-specific reporter cells, TCR-dependent signaling can be quantified based on luminescence. The ability of a given Nef sequence to downregulate HLA-I on the target cell thus correlates inversely with the TCR-mediated luminescence signal in effector cells.

We first undertook the following control experiments. Target cells expressing either A02 or A02_{GG,ΔCKV} were pulsed with increasing concentrations of FK10 peptide and cocultured with A02-FK10-specific reporter cells, and the TCR-mediated signal was quantified by measuring luminescence (Fig. 6A). As expected, the luminescence intensity correlated positively with increasing FK10 peptide concentrations in both A02 and A02_{GG,ΔCKV} target cells. Moreover, the magnitudes of luminescence generated by effector cells were comparable regardless of whether A02 or A02_{GG,ΔCKV} target cells were used (Fig. 6A). This suggested that A02 and A02_{GG,ΔCKV} target cells were equally sensitive to recognition by A02-FK10-specific TCR. Importantly, no response was observed when parental target cells lacking HLA-A*02:01 were pulsed with FK10 peptide, confirming the HLA- and antigen-specific nature of the assay (Fig. 6A). Next, target cells were infected with HIV-1 NL43-Nef_{SF2} and NL43-ΔNef and incubated with effector cells at various effector/target (E/T) ratios (Fig. 6B). Effector cells cultured in the presence of A02 and A02_{GG,ΔCKV}

target cells infected with HIV-1 NL43-ΔNef generated much greater luminescence signals than those cultured with control parental target cells lacking HLA-A*02:01. Furthermore, A02 and A02_{GG,ΔCKV} target cells stimulated luminescence signals in effector cells with comparable magnitudes across all E/T ratios examined (Fig. 6B). In contrast, the effector cell responses were dramatically decreased when target cells were infected with Nef_{SF2}-expressing HIV-1 (Fig. 6B). Together, the results of these control experiments indicated that A02 and A02_{GG,ΔCKV} target cells were similarly functional as target cells and that wild-type Nef_{SF2} expression could substantially reduce T-cell recognition of HIV-infected cells.

We then tested effector T-cell responses following coculture with target cells infected with HIV-1 expressing Nef_{SF2} or CP66-Nef or their respective Nef-202 mutants. The effector T cell responses toward these Nef-positive (Nef⁺), HIV-infected cells were quantified by luminescence and normalized to the responses generated against HIV-1-ΔNef-infected target cells. Consistent with the results of the control experiments, the effector T cell responses to A02 and A02_{GG,ΔCKV} target cells infected with HIV-1 Nef_{SF2} (encoding Tyr-202) were comparable in magnitude (Fig. 6C). In contrast, the responses to A02_{GG,ΔCKV} target cells infected with HIV-1 Nef_{SF2} encoding the His-202 mutation were significantly higher than the responses to A02 target cells infected with this virus (*t* test, *P* = 0.0039) (Fig. 6C). Furthermore, while the responses to A02 and A02_{GG,ΔCKV} target cells infected with the

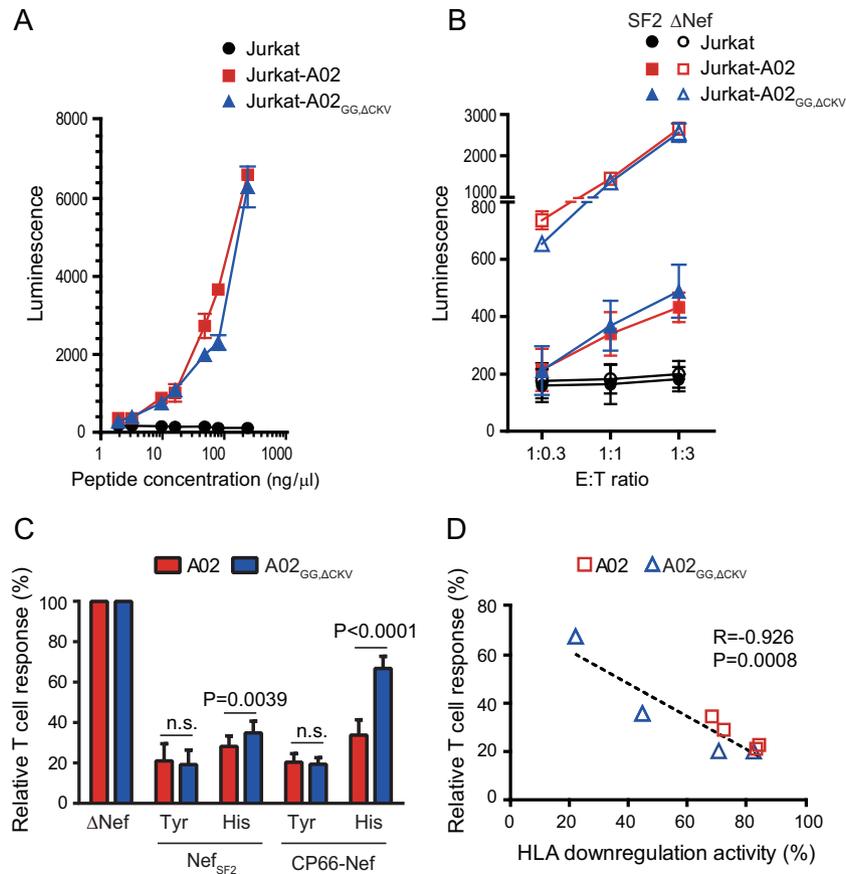


FIG 6 Effects of differential levels of Nef sensitivity to HLA-A and HLA-B on antigen-specific TCR recognition. (A) Luciferase-reporter effector T cells expressing an HLA-A*02-restricted HIV-1 Gag FK10-specific TCR were incubated with parental Jurkat target cells or Jurkat cells stably expressing A02 or A02_{GG,ΔCKV} in the absence or presence of increasing concentrations of synthetic FK10 peptide at an E/T ratio of 1. T cell recognition is shown by the luminescence intensity detected at 6 h. (B) The same effector cells were incubated with parental Jurkat target cells or those stably expressing A02 or A02_{GG,ΔCKV} that were infected with HIV-1 encoding Nef_{SF2} or ΔNef at an E/T ratio of 1:0.3, 1:1, or 1:3. T cell recognition is shown as the luminescence intensity detected at 6 h. (C) The same effector cells were incubated with parental Jurkat target cells or those stably expressing A02 or A02_{GG,ΔCKV} that were infected with HIV-1 encoding Nef_{SF2} or CP66-Nef or their indicated residue 202 mutants. The relative T cell response was calculated as the luminescence intensity at 6 h, normalized to that of target cells infected with NL43_{ΔNef} (set to 100%). (A to C) Data shown for all panels represent the mean results \pm SD from 3 to 5 independent assays. Statistical analysis was performed by paired *t* test. n.s., not significant. Over all experiments, the background luminescence intensity obtained by incubation of the effector cells alone was 141.5 ± 20.2 , and the frequency of HIV-infected cells within the target cell population as determined by intracellular expression of the p24^{Gag} protein was $45.7\% \pm 8.9\%$. (D) Correlation between relative T cell response and Nef's HLA downregulation activity in both A02- and A02_{GG,ΔCKV}-expressing cells infected with HIV-1 encoding Nef_{SF2} or CP66-Nef or their respective Nef-202 amino acid variants. Data for the relative T cell response and Nef's HLA downregulation activity are derived from the results shown in Fig. 6C and 4B, respectively. Statistical analysis was performed by Pearson's correlation analysis.

HIV-1-CP66-Nef (Tyr-202) revertant virus were comparable in magnitude and similar to those induced by Nef_{SF2}, we observed significantly greater T cell responsiveness toward A02_{GG,ΔCKV}-expressing target cells infected with HIV-1 encoding the parental CP66-Nef (i.e., carrying the natural polymorphism His-202) than toward A02 target cells infected with the same virus (*t* test, $P < 0.0001$) (Fig. 6C). Moreover, the magnitude of responses against the parental HIV-1-CP66-Nef virus was higher in both cells than in cells infected with HIV-1 strains encoding Nef_{SF2} or the CP66-Nef (Tyr-202) revertant. Finally, the T cell responses as measured in this assay and Nef's HLA-I downregulation activity as measured by flow cytometry showed a significant inverse relationship (Pearson's correlation coefficient, $r = -0.926$, $P = 0.0008$) (Fig. 6D). Together, these results are consistent with our observation that the naturally occurring His-202 mutation attenuates Nef's ability to downregulate HLA-I, with a more pronounced impairment seen for HLA-B (modeled herein by the A02_{GG,ΔCKV} construct) than

for HLA-A. Our results further suggest that inefficient removal of HLA-B from the infected cell surface preferentially renders these cells more detectable by HIV-specific, HLA-B-restricted effector T cells.

DISCUSSION

In this study, we assessed the interplay between naturally occurring host (HLA-I) and virus (HIV-1 Nef) polymorphisms. We observed that HLA-B cytoplasmic tails displayed significantly decreased susceptibility to downregulation by primary HIV-1 Nef clones compared to the susceptibility of HLA-A cytoplasmic tails. On the host side, the relative resistance of HLA-B to downregulation by patient-derived Nef clones appeared to be modulated by the GG_{314,315} motif and/or the lack of the C-terminal CKV₃₃₉₋₃₄₁ motif in the HLA-B cytoplasmic tail. On the viral side, HIV-1 Nef codon 202 was responsible, at least in part, for differential downregulation of HLA-A and HLA-B allotypes by this protein. Impor-

tantly, the results from our TCR recognition assays indicated that the differential susceptibilities of HLA-I molecules to downregulation by patient-derived Nef clones are likely to modulate T cell recognition of HIV-infected target cells presenting viral antigens in complex with HLA-I on their surface.

While it has long been known that HLA-B-restricted T cell responses exert a dominant influence on HIV-1 immune control (38, 39), it was only recently that the relative resistance of HLA-B to Nef-mediated downregulation was put forward as a possible underlying mechanism (23). The present study extends the previous work, which was performed using laboratory-adapted HIV-1 reference strains, by demonstrating that the majority of naturally occurring Nef sequences also downregulate HLA-A to a greater degree than HLA-B. Our results thus identify differential levels of susceptibility to HLA-A and HLA-B as a fundamental property of HIV-1 subtype B Nef sequences.

The introduction of various amino acid substitutions at Nef codon 202 (wild-type Tyr) substantially affected the protein's ability to downregulate HLA-I, with greater impairment of HLA-B downregulation than of HLA-A downregulation. In particular, the uncommon natural variants Leu and His and the unnatural variant Ala displayed this phenotype, while the common natural variant Phe conferred only modest effects compared to the activity of Nef with the wild-type Tyr. This provides a possible explanation for the relative frequency of these residues in natural subtype B HIV-1 Nef sequences. Of interest, the Nef Phe-202 polymorphism has been identified as being associated with host expression of HLA-A*30:01 and HLA-B*15:01 (40), suggesting that it may arise under immune selection pressure by these alleles *in vivo*; however, we were unable to confirm this experimentally due to limited availability of peripheral blood mononuclear cells (PBMC) from this cohort. Also of interest, while Tyr and Phe are frequently observed at Nef codon 202 in all HIV-1 group M subtypes, the consensus at this residue in HIV-1 group O is Leu (Los Alamos HIV-1 sequence database). Given our observation that the Leu-202 substitution in Nef_{SF2} substantially increased the HLA-A/HLA-B downregulation ratio (Fig. 3B), it would be intriguing to investigate downregulation of HLA-I molecules by naturally occurring HIV-1 group O Nef sequences.

Some limitations of this study merit mentioning. Although we investigated 46 patient-derived HIV-1 subtype B Nef clones, this panel of sequences did not capture the entirety of HIV-1 subtype B Nef genetic diversity. Nevertheless, this relatively small subset of patient isolates exhibited a substantial dynamic range of HLA-A and HLA-B downregulation function. Importantly, the majority of Nef clones were less able to downregulate HLA-B than HLA-A—an observation that remained true for all cell lines and primary T lymphocytes, as well as all individual HLA alleles and cytoplasmic variants tested. As our goal was to investigate Nef-mediated HLA-A and HLA-B downregulation on the surface of HIV-infected cells, we employed recombinant virus approaches (as opposed to transient-transfection systems, which are limited by Nef overexpression and potential cytotoxicity during plasmid delivery). Nevertheless, recombinant approaches are inherently limited by potential incompatibilities between the insert and the backbone (though all of the recombinant viruses used were replication competent and demonstrated Nef polyfunctionality in various cell lines and primary T cells, as demonstrated in a previous published study of these clones [41]). The crystal structure of a ternary complex formed by Nef, the HLA-A02 cytoplasmic tail,

and the cargo-bonding μ 1 subunit of AP1 was recently solved (37), yielding new insight into the molecular basis of Nef-mediated HLA-I downregulation function. However, due to the disordered nature of the C-terminal end of the HLA-A02 cytoplasmic tail, this region was not included in the structure (37), rendering it impossible to directly investigate interactions between this region (notably, the C-terminal CKV_{339–341} motif) and Nef-202. Nevertheless, modeling of a 7-amino-acid spacer following Gly-331, the final residue of the HLA-A02 cytoplasmic tail observed in the structure, indicated that the CKV_{339–341} motif could readily be positioned next to the side chain of Nef Tyr-202, supporting a possible interaction.

Despite these limitations, our study extends the current understanding of Nef-mediated HLA-I downregulation function by demonstrating that, on average, subtype B Nef sequences from untreated, chronically HIV-infected patients downregulate HLA-A ~1.25-fold more efficiently than HLA-B. Moreover, these effects appear to be modulated, at least in part, by polymorphisms at Nef residue 202, as well as those located within the HLA-I cytoplasmic domain. Importantly, the differential levels of Nef-mediated HLA-A and HLA-B downregulation on HIV-infected cells modulate their subsequent recognition by HIV-specific T cells. Together, these results identify a new motif in HIV-1 Nef that differentially alters its ability to counteract HLA-A- and HLA-B-restricted CTL responses. Further studies will be necessary to determine whether Nef polymorphisms at residue 202 are associated with variations in immune-mediated control of infection or viral pathogenesis.

MATERIALS AND METHODS

Patient-derived Nef clones and recombinant virus preparation. The recombinant viruses expressing patient-derived Nef clones in an HIV-1 NL43 proviral backbone were generated as part of previously published studies (28, 30, 41). Briefly, Nef sequences were isolated from plasma viral RNA of 46 individuals chronically infected with HIV-1 subtype B, recruited in the Boston area, who were untreated at the time of sample collection and had a median plasma viral load of 80,500 (IQR, 25,121 to 221,250) RNA copies/ml and a median CD4 count of 292.5 (IQR, 72.5 to 440) cells/mm³, as described previously (30, 42, 43). This study was approved by the Institutional Review Boards at all relevant institutions, and all participants provided written informed consent. The GenBank accession numbers for clonal *nef* sequences used in this study are JX440926 to JX440971 (41). To facilitate a consistent codon numbering scheme (based on the sequence of the Nef_{HXB2} reference strain), all clonal Nef sequences were pairwise aligned to that of Nef_{HXB2} and insertions stripped out. Patient-derived *nef* clones isolated as described above were transferred into plasmid pNL43 and confirmed by sequencing as described previously (41). In addition, specific mutations (i.e., at Nef codons at 158 and 202) were introduced into the *nef* clone of strain SF2 using conventional overlapping PCR (33, 35), and the entire *nef* sequence was reconfirmed after subcloning into pNL43. The resultant DNA (5 μ g), along with a plasmid encoding vesicular stomatitis virus envelope glycoprotein (VSV-g) (1 μ g), was transfected into 10⁶ 293T cells, and the virus-containing culture supernatants were harvested 48 h later. Recombinant viruses harboring *nef* from HIV-1 subtype B reference strain SF2 (Nef_{SF2}) or lacking *nef* (Δ Nef) were used as positive and negative controls, respectively, as previously described (30, 35).

Cells and antibodies for HLA analysis. Nef-mediated downregulation of cell surface expression of HLA-I molecules was assessed using the following four different cell systems: (i) 721.221, an HLA-A, -B, and -C-null human lymphoblastoid cell line, which was transfected to express a single HLA-I allele; (ii) T1, a human CD4⁺ monocytic cell line that expresses 6 different autologous HLA-I alleles (2 alleles each of HLA-A, -B,

and -C); (iii) human primary T lymphocytes isolated from HIV-negative donors expressing autologous HLA-A*02 and HLA-Bw6 serotype alleles; and (iv) Jurkat, a human CD4⁺ T cell line that was stably transfected with genes encoding HLA-A*02:01 or its cytoplasmic tail mutant. For the first system, we used the HLA-A, -B, and -C-null 721.221 cell line (44) that had been engineered to stably express a single HLA class I allele encoding HLA-A*02:01, HLA-A*24:02, HLA-A*33:03, HLA-B*35:01, HLA-B*57:01, or HLA-C*04:01. These transfectants were kindly provided by M. Takiguchi, Kumamoto University, Japan, or T. Yamamoto, Vaccine Research Center, NIH, United States. HLA-I expression for each of the 721.221 lines was validated by HLA genotyping methods as described previously (45), and HLA-I cell surface expression was confirmed by staining with a pan-HLA-I-specific antibody (clone w6/32; BioLegend Co.), followed by flow cytometry. For the second system, the human CD4⁺ monocytic cell line T1 was used. The HLA-I genotyping results for T1 cells were A*02:01, A*31:01, B*40:01, B*51:01, C*01:02, and C*03:04. In the case of T1 cells, the cell surface expression of the specific HLA-I alleles HLA-A*02:01 and HLA-B*51:01 was evaluated using an HLA-A2 serotype-specific MAb (clone BB7.2; BioLegend) and an HLA-Bw4 serotype-specific MAb (clone TU109; kindly provided by M. Takiguchi), respectively. For the third system, primary T lymphocytes were isolated from PBMC of HIV-negative donors, followed by activation with phytohemagglutinin for 5 days. For the fourth system, the human CD4⁺ Jurkat T cell line was used. Human cDNA encoding HLA-A*02:01 was cloned from PBMC of a healthy HLA-A*02:01-positive volunteer into plasmid pcDNA3.1. Mutations (DR_{314,315} to GG_{314,315} and deletion of CKV₃₃₉₋₃₄₁) were introduced into the cytoplasmic tail region of HLA-A*02:01, giving rise to HLA-A02_{GG,ΔCKV}, in which the cytoplasmic tail region is equivalent to that of HLA-B*35:01. In all cases, the levels of cell surface expression of HLA-A02 and its cytoplasmic tail mutant were evaluated by an HLA-A2 serotype-specific MAb as described above.

HLA-I downregulation assay. The 721.221, Jurkat, T1, and primary T cells were infected with the VSV-g-pseudotyped recombinant HIV-1 and harvested 48 h later for staining with a pan-HLA-I-specific antibody (clone w6/32; BioLegend Co.) or the serotype-specific MAbs, followed by 7-amino-actinomycin D (BioLegend Co) staining and intracellular p24^{Gag} staining with anti-p24 Gag-fluorescein isothiocyanate MAb (KC57; Beckman Coulter) as previously described (30). Live cells (negative for 7-amino-actinomycin D) were gated, and HLA-I expression in p24⁺ and p24⁻ subsets was analyzed by flow cytometry (FACS-Canto II or FACSVers; BD Biosciences). For calculation of the HLA-I downregulation activity by Nef, the following formula was used (where MFI is mean fluorescence intensity): (MFI of HLA-I in p24⁻ subset – MFI of HLA-I in p24⁺ subset)/MFI of HLA-I in p24⁻ subset.

T cell recognition assay. The effects of Nef-mediated HLA-I downregulation on T cell recognition were analyzed using a T cell receptor (TCR)-based reporter cell assay as previously described (46, 47). Briefly, the effector cells were prepared by electroporation of Jurkat cells with expression plasmids encoding TCR- α and - β chains specific for the HLA-A*02:01-restricted HIV-1 Gag FK10 epitope (Gag₄₃₃₋₄₄₂ [FLGKI-WPSYK]), human CD8- α chain (InvivoGen), and NFAT-luciferase reporter (Affymetrix). The resultant cells were incubated for 24 h, followed by separation of the CD8-expressing fraction by magnetic bead sorting (Miltenyi). Target cells were prepared by infection of parental Jurkat cells (lacking A02) or Jurkat cells transfected with A02 or A02_{GG,ΔCKV} with recombinant HIV-1 encoding *nef* alleles of interest. For control experiments, uninfected target cells were pulsed with the synthetic FK10 peptide. Effector cells (5×10^4 cells) were cocultured with target cells (5×10^4 cells, unless otherwise specifically indicated) for 6 h and then harvested for the luciferase assay (Steady-Glo luciferin kit; Promega). Luminescence was measured by using a plate reader (CentroXS3; Berthold Technologies) with the following conditions: 3,000 ms integration and 100 ms settle time.

Western blotting. HEK-293T cells were transfected with proviral DNAs encoding Nef_{SP2} or mutants for preparation of cell lysates as described previously (30, 31). Briefly, lysates were prepared in duplicate, subjected to SDS-PAGE, transferred to nitrocellulose membranes, and stained with rabbit anti-Nef polyclonal antiserum (NIH AIDS Research and Reference Reagent Program), followed by secondary enhanced chemiluminescence rabbit IgG (horseradish peroxidase-linked whole antibody; GE Healthcare Life Sciences), as reported previously (30). Band intensities were quantified using the Amersham Imager 600 (GE Healthcare Life Sciences).

Statistical analysis. Statistical analyses were performed using Graph Pad Prism 6.0. For Nef codon function analyses, the Mann-Whitney *U* test was used to identify amino acids associated with differential abilities to downregulate HLA-A and HLA-B (expressed as HLA-A/HLA-B downregulation ratios). Multiple comparisons were addressed using *q* values, the *P* value analogue of the false discovery rate (FDR), which denotes the expected proportion of false positives among results deemed significant at a given *P* value threshold (48). For example, at a *q* value of ≤ 0.2 , we expect 20% of identified associations to represent false positives. In the present study, statistical significance was defined as a *P* value of < 0.05 (for univariate analyses) or a *P* value of < 0.05 and a *q* value of < 0.2 (for analyses correcting for multiple hypothesis testing).

SUPPLEMENTAL MATERIAL

Supplemental material for this article may be found at <http://mbio.asm.org/lookup/suppl/doi:10.1128/mBio.01516-15/-/DCSupplemental>.

Figure S1, EPS file, 0.5 MB.

Figure S2, EPS file, 0.8 MB.

Figure S3, EPS file, 0.6 MB.

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